

Fig.

Fig.

ICTB : 1	ATGACTGTCTGGCAAACCTGACTTTCGCTGTTGGCAGCCTGC-GAGCTTGGGGCTCCAGGCCACAGC 60 (SEQ ID NO:2)
SLR : 13	ATCTCTATCTGGCGATCGCTGATGTTGGGGTTTCCCCCAGGAATGGGGCGGGC 72 (SEQ ID NO:4)
ICTB : 61	AgtTTCTGGCATCGGCTGTTGGCAGCCTGC-GAGCTTGGGGCTCCAGGCCACAGC 119
SLR : 73	AgtGTGGCTCCATCGTTGGCTGGCACAGAG-TGGATAACAGCTAGTGTGCTCTG 131
ICTB : 120	GCTTGGCTCTGAGGCACTGGT--GGCTTCTGCTGCTACGGTTGGCTCCG 177
SLR : 132	GCCCCACTTCGAGGCAATTGGTACGGCT-CTAG-TGGCAATAATTGGGGCTCCC 189
ICTB : 178	TttTGTGCCAGTTCGCCCTAGGGTTGGGCTAGCCGGATCCGG-GCCTATTGGGCCCT 236
SLR : 190	TtCACCTCACCACTATGGCATTTTAT-GCTGCTCTGTGGAGCCCTTGGCTCT 248
ICTB : 237	GCTCTCGCTGACAGATACTGATCTGGGAAAGCA---ACCCCATTCACTGGCTGGCT 293
SLR : 249	GCTGACCTTGCTGAT--CAACCAAG-GAAGGGTTGACTCCATCCATTGGTTT 305
ICTB : 294	GCTCTACTGGGGCTGATGCCAACCGGACTCTCACCCGTACCGCTGGCTGGTT 353
SLR : 306	TGGCTACTGGTCATTGGCAATTAAAGCTAAATTATGTCGTTCTCCGGTAAGGGCGGGC 365
ICTB : 354	AGTTGGGCTAGCCAACGTGAC-GCTC-TACCTGTTGGCTGGCTGGCTGGTT 411
SLR : 366	GtGGGGTTAGCGAAATTAAAGCTAAATTATGTCGTTCTCCGGTAAGGGCGGGT 423
ICTB : 412	CTCCGCAATTCCCGTCTGC-GATCGCTGCTGTTCTGGCTCGTACATCGCTTT 470
SLR : 424	TTGGCAAAACAAACATGGTGAAC-CGGTTAGTAACCGTTGTTACTGGTAGGGCTATT 482

Fig. 2

ICTB :	471	TGTCAAGTGTCTACGGCCTAACCAAATGGATCTACGGGTTAGAGAGCTGGGACTTGGGT	530
SLR :	483	GGGGGAGTTACGGTCTGCACAAACAGTTGACGGGTTAGAACAGTTCAGCTGGAA	542
ICTB :	531	GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTACAGCTATCTGGCAACCCCAA	590
SLR :	543	TGACCCCACCTCTACCTTGCCCCAGGCCACTAGGGTATAAGCTTTAGGTAATCCCAA	602
ICTB :	591	CCTGCTGGCTTATCTGGCGGACTGCCCTT-CTGCACGGCATGGGTGT	649
SLR :	603	TCTCTGGGGCTTACCTGGCCATGACGGTTAGCTTGAGCTTGAGT-GCCCTGGGTAT	661
ICTB :	650	GGCGGGCTGGCTCCAAAGCTGGCGATCG-CTGCGCACGGTGGAGCCAGCTTATGT	708
SLR :	662	GGCGACGGTGGGCCAAACTGCTGG-GAGCAACCATTGGTATGTTAACCTACTCTGT	720
ICTB :	709	CTGATCCTCACACTGGCTGGCTGGCTGGGATGATTGGCTGGCCATGATTGGCTGG	768
SLR :	721	CTCTTTTACCCAGGGGGGGCTAGCAGTGGCTAGGAGTGTGGGAGCTACCTTC	780
ICTB :	769	GCGTTATTAGGGCTRACTGGTTCAACCCGGCTACCCGACGGCTGGCTA	828
SLR :	781	CTGGCCCTTGTACTCTGGTGTACCCAAATTACCCAAATTGGCAACGGTGGCT	840
ICTB :	829	TTCCCAAGTGTATTGGGGACTAGTGGCTAACCCGGCTACCCGACGGCTGGACT---	884
SLR :	841	TTGCCCTGGC---GATGCC---GATGCC---GATGCC-TATATTAGGTGGGGAGGCTTGATTGGCG	894
ICTB :	885	-TG-AGCCGGTGTGCCGGTGTGAGCATCTTGTGGGGCTGAAGACAGCAGAAC	942
SLR :	895	GTGGAACCGGATTGACTCAGGGCATGAGCATTTTGTGGGGAAAGACAGCAGTAAT	954

Fig. 2
(Continued)

ICTB	943	AACTTCCGGATCAATGTCCTGGGTGGCTGCAGATGATTCAAAGATGGGCCCTGGCTG	1002
SLR			1074
ICTB	1003	GGCATCGGGCGGAATAACGCCCTTAACCTGGTTATCCCTCTATCACAGGGCGGC	1062
SLR			
ICTB	1015	GGCATTGGCCATCAATGTCCTGGGAAGGGTAAAGCCATGATCCGAGCCCTATCART	
SLR			1074
ICTB	1063	TTTACGGCGTTGAGCGCTACTCCGTCCGGCTGAAGTCGGGGTGAAGTGAGGGGACTACTG	1122
SLR			
ICTB	1075	TTCACCCGCCCTGAGTGCTTACCTAGAAATTGGTGGAAACGGGTAGTT	1134
SLR			
ICTB	1123	GGCTTGA-CGGCCTTCGCTTGCT-GCTGGTCAAGGGGTGACGGGGTGGCAGG	1180
SLR			
ICTB	1135	GGTTTTACCTGTATGCTC-TGGCTGGTGGCGTTACCCTAGGCAAAGGC-GTAGAACTGG	1192
SLR			
ICTB	1181	TGAGGCCACTGGGGCGATGCCAATCCCC--AAGCCCTTTGGTGTATGGCTAGCTTGGC	1238
SLR			
ICTB	1193	TTAACCG-CTGTCGC-CAAAACCTCGCCCCGAAGGCATCTGGATTATGGGGCTTTCAGC	1250
SLR			
ICTB	1239	CGGTTGGCAGGAATGCTGGGTCAACGGTCTGGTGTATGGGAGCTATGGACGGGAGGC	1298
SLR			
ICTB	1251	GGCGATCATCGGTTGGTCCACGGCATGGTAGATACAGTCTGGTACGGTACGGGGCTTGG	1310
SLR			
ICTB	1354	CCTTCCAAGCAACTCCCTCCAGAAGCCGAGCATTCAGACGAA	1395
SLR			
ICTB	1369	GCCCGTTTGAGGGCACTAAAGAA---GAAATGAGGACAAA	1407

Fig. 2
(Continued)

SLR : 5	ISIWRSLMFGFSPQEWGRGSVLIQASVLUKWPHEALGTALVALIFIRAPP	64
ICTB : 61	PVSSAALGLGLARIAAYWALLSLLTDIDLROATPIHMLVLYMVGVDALATGLSPVYRADALYVG	120
	++ LG+ + PQ+WG S LRRL G +W +S L + EALG L+A++ +APP	
SLR : 65	TSTTMGLGIFMLLCGAFAWLITFADQPCKGLTPIHVLVFAYMCSAIAVGFSVPVKMAASG	124
ICTB : 121	LAKLTLYLVFALAARVLRNPRLLSLLFSSVVITSLFVSVYGLNQWIYGVEEELATWVDRN	180
	LAKLT L +F LAAR+L+N + L +W++ L V YGL Q + GVE+LATW D	
SLR : 125	LAKLTANLCLFLLAARLILQNKQWLNRLLTVVLLVGLLIVGSYGLRQQVQDGEQLATWDRDPT	184
ICTB : 181	SVADFTSRVSYLSYLGNPMLAAYLVPTTAFSAAAIGWWRGWLPKLLIAATGASSLCLILT	240
	S +RVYS+LGNPMLAAYLVP T S +A+ VWR W PKLL + LCL T	
SLR : 185	STLAQATRVYSFLGNPNMLAAYLVPMTGSLSLSAVTVRRWWPKLIGATMVIVNLCLFFT	244
ICTB : 241	YSRGCGWLGFWAMIFWAWLLGLYWFQPRRLPAPWPRRMWLPVVLGGLVAVVLLAVGLEPLRY	300
	SRGGWL +A+ + L +W+ P+LP W+RN P+ + V + A++ +EP+R+	
SLR : 245	QSRGCGWLAVALAGATFLALCYFWLWLQPLFKFWQRWSLPLAIAVAVILGGALIAVEPIRL	304
ICTB : 301	RVLSIFVGREDSNNFRINWLVLAQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTALSA	360
	R +SIF GREDDSSNNFRINW V MI+ RP +GIGPN AFN +YP Y + RFTALSA	
SLR : 305	RAMSIFAGREDSNNFRINWEGVKAMIRARPIIGIGPGNEAFNQIYPPYYMRPFTALSA	364
ICTB : 361	YSVPLEVAVEGGLLGLTAFAWLLVTAVTAVRQVSRLRDRNPQAFLMASLAGLAGMLG	420
	YS+ LE+ VE G+G T WLL VT V V R R+ P+ W+M +LA + G+L	
SLR : 365	YSIVLBILVETGVVGFTCMWLMLLAUTLGKGVELVKRCQTLAPEGIWIMGALAIIGLLV	424
ICTB : 421	HGLFDTVLVRPEASTLWILCIGAIAASFWQOPSKQLPPEAEHSDEKM	467
	HG+ DTV YRP STLWIL + AS W ++ + E+ D+ +	
SLR : 425	HGMVDTWYRPPVSTLWILLVAIVASQWASAQARLEASKEENEDKPL	471

3
Fig.

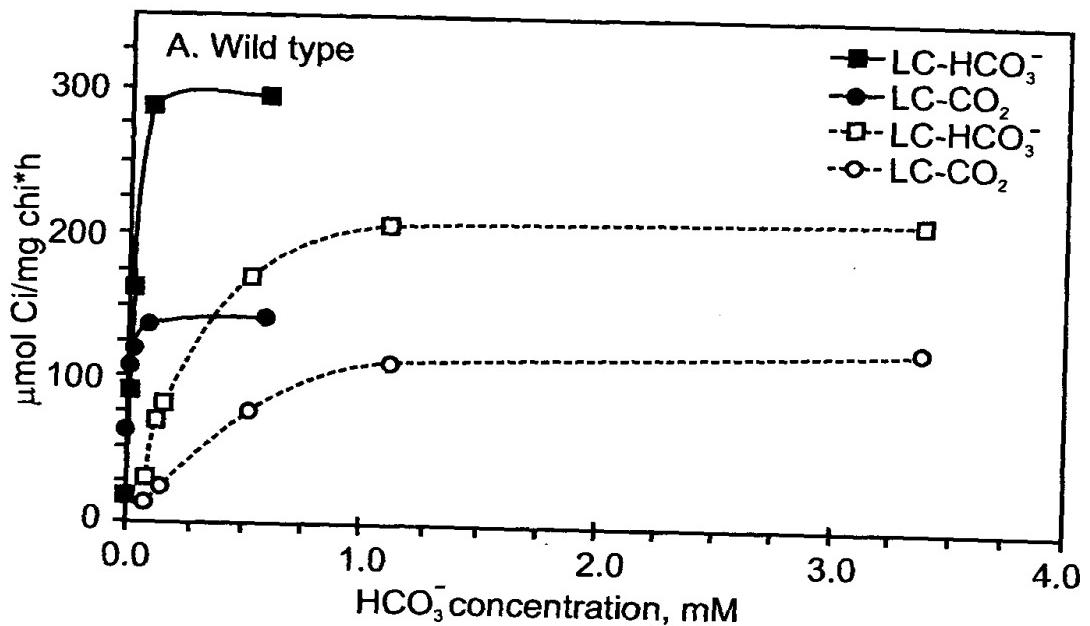


Fig. 4a

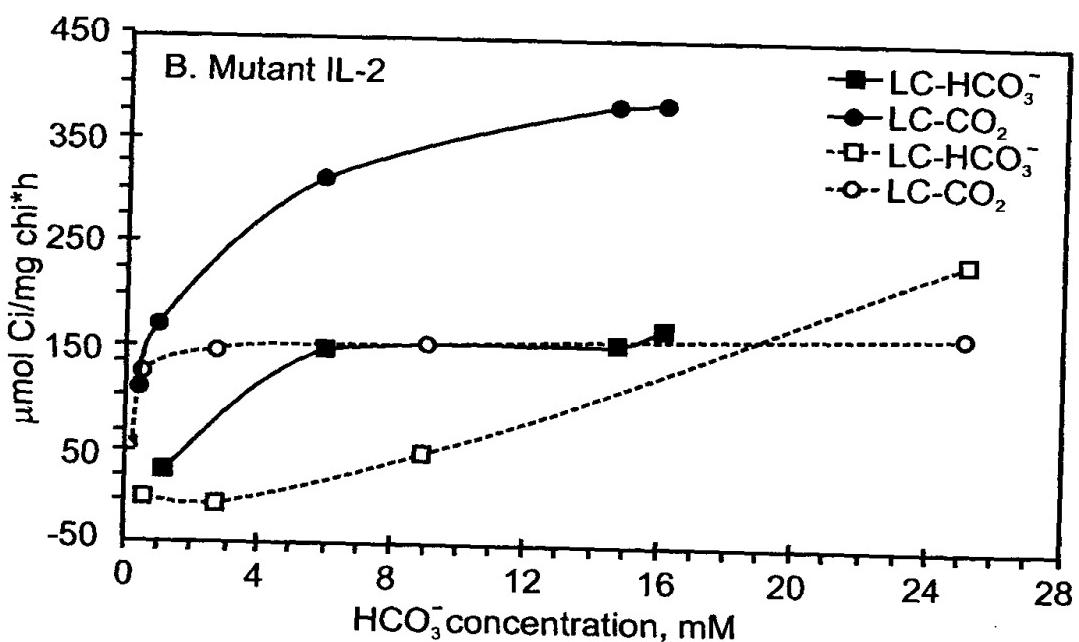


Fig. 4b

Wild type GGGCT-AGCCCGGA'TCGCGGCCATTGGGCC (SEQ ID NO: 6)
IL-2 ApaI side GGGCT-AG--G-GATCGC-GCCTATTGGCCC (SEQ ID NO: 7)
IL-2 BamHI side GGGCTCA---GATCGC-GCCTATTGGCCC (SEQ ID NO: 8)
IctB G L A A I A A Y W A L (SEQ ID NO: 9)

Fig. 5

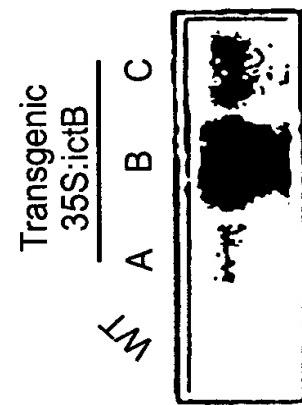


Fig. 6